OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.3
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Run on: December 9, 2002, 10:46:24 ; Search time 61 Seconds
                                           (without alignments)
                                           2135.042 Million cell updates/sec

Title: US-09-765-034-2
Sequence: 1 MLGIMAWNATCKNWLAAEAA..........KSLTSFSRWAHELLSFREK 334
Perfect score: 1747

Scoring table: BLOSUM62
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                Ygapop   10.0 , Ygapext   0.5
                Fgapop   6.0 , Fgapext   7.0
                Delop   6.0 , Delext   7.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
Published_Applications_NA:*
 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Database :
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-Q=/cgn2_1/USPTO_spool/US09765034/runat_05122002_132013_21353/app_query.fasta_1.519
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09765034 @CGN_1_1_21_@runat_05122002_132013_21353
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	477	27.3	1014	10	US-09-943-798-3	Sequence 3, Appli
2	395.5	22.6	831	10	US-09-943-798-1	Sequence 1, Appli
3	384	22.0	993	10	US-09-826-791-1	Sequence 1, Appli
4	384	22.0	1041	9	US-09-828-478-1	Sequence 1, Appli
	384	22.0	1041	10	US-09-826-791-5	Sequence 5, Appli
	384	22.0		10	US-09-866-230-6	Sequence 6, Appli
	384	22.0		10	US-09-828-478-3	Sequence 3, Appli
	346.5	19.8		10	US-09-728-952-26	Sequence 26, Appl
	338	19.3		10	US-09-728-422-1	Sequence 1, Appli
	338	19.3		10	US-09-788-133-1	Sequence 1, Appli
	336.5	19.3		10	US-09-880-107-10158	Sequence 10158, A
	336.5	19.3		10	US-09-864-761-26799	Sequence 26799, A
	331	18.9		9	US-09-864-761-10158	Sequence 10158, A
	326.5	18.7		10	US-09-880-261-1	Sequence 1, Appli
	323	18.5		10	US-09-852-156-7	Sequence 7, Appli
	323	18.5		10	US-09-967-768A-296	Sequence 296, App
	321.5	18.4		10	US-09-880-107-3034	Sequence 3034, Ap
	317.5	18.2		10	US-09-962-832-218	Sequence 218, App
	317.5	18.2		10	US-09-944-807-20	Sequence 20, Appl
	314	18.0		10	US-09-852-156-9	Sequence 9, Appli
	312.5	17.9		9	US-10-120-394-19	Sequence 19, Appl
	312.5	17.9		10	US-09-837-446-1	Sequence 1, Appli
	312	17.9		10	US-09-214-904-5	Sequence 5, Appli
	311.5	17.8		12	US-10-084-206-1	Sequence 1, Appli
	311	17.8		10	US-09-852-156-11	Sequence 11, Appl
	309	17.7		10	US-09-962-832-239	Sequence 239, App
	309	17.7		10	US-09-954-456-1593	Sequence 1593, Ap
	306	17.5		10	US-09-900-699A-1	Sequence 1, Appli
	304.5	17.4		9	US-09-104-792-1	Sequence 1, Appli
	303	17.3		10	US-09-789-482-3	Sequence 3, Appli
	303	17.3		10	US-09-789-486-3	Sequence 3, Appli
	303	17.3		10	US-09-954-456-267	Sequence 267, App
	303	17.3		10	US-09-954-456-945	Sequence 945, App
	303	17.3		10	US-09-954-456-1588	Sequence 1588, Ap
	302	17.3		10	US-09-944-807-1	Sequence 1, Appli
	301.5	17.3		10	US-09-852-156-5	Sequence 5, Appli
	301.5	17.3		10	US-09-852-156-3	Sequence 3, Appli
	301.5	17.3		10	US-09-852-156-1	Sequence 1, Appli
	301	17.2		10	US-09-931-381A-15	Sequence 15, Appl
	300.5	17.2		10	US-09-880-107-1611	Sequence 1611, Ap
	300.5	17.1		10	US-09-964-824A-100	Sequence 100, App
	299.5	17.1		12	US-10-106-623-3	Sequence 3, Appl
	299.5	17.1		9	US-10-001-833-29	Sequence 29, Appl
	298.5	17.1		10	US-09-940-063-1	Sequence 1, Appli
	298.5	17.1		10	US-09-997-522-1	Sequence 1, Appli
	297	17.0		10	US-09-804-551B-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-943-798-3

Sequence 3, Application US/09943798
Patent No. US20020065215A1
GENERAL INFORMATION:
  APPLICANT: Glaxo Group Limited
  TITLE OF INVENTION: Polypeptide
  FILE REFERENCE: QG1021
  CURRENT APPLICATION NUMBER: US/09/943,798
  CURRENT FILING DATE: 2001-08-31
  NUMBER OF SEQ ID NOS: 4
  SEQ ID NO 3
  LENGTH: 1014
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-943-798-3

SOFTWARE: FastSEQ for Windows Version 3.0

Alignment Scores:
Pred. No.:   2.5e-41
Score: 477.00
Percent Similarity: 55.88%
Best Local Similarity: 35.95%
Query Match: 27.30%
DB:

US-09-765-034-2 (1-334) x US-09-943-798-3 (1-1014)

Length: 1014
Matches: 110
Conservative: 61
Mismatches: 123
Indels: 12
Gaps: 6

; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-798-1

US-09-765-034-2 (1-334) x US-09-943-798-1 (1-831)

Alignment Scores:
Pred. No.:
Score: 7.24e-33
                         395.50   Length: 831
Percent Similarity: 55.73%   Matches: 92
Best Local Similarity: 35.11%   Conservative: 54
Best Local Similarity: 22.64%   Mismatches: 109
Query Match: 10   Indels: 7
DB: Gaps: 5

Qy   52 LeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAla   71
          ::::::: ||| |||||| :::: || ||||||||::: ||||||||
Db   1   ATCAGACCTTGGGAAGCAGCACCACCATCATTATATGCTGAACCTGGCCTGCACAGAATCGCTG   60

Qy   72 PheLeuCysThrLeuProMetLeuIleLeuArgSerTyrAlaAsnGly--AsnTrpIleTyr   90
          |||||||:::|| |||||||::: |||:||||| :::|| ||||||||::
Db   61 TAYCTGACCAGCCTCCCCTTCCCTGATTCACTACTACTATGCCAGTGGCGAAAATGGATCTTT   120

Qy   91 GlyAspValLeuCysIleSerAsnArgThrValLeuHisAlaAsnLeuThrTyrThrSerIle   110
          |||||| |||::: ||| ||||||||| |||||||||||::::||||||||
Db   121 GGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCAGTTCAATTCAAACCTGTATAGCGATC   180

Qy   111 LeuPheLeuThrPheIleSerIleAspArgTyrLeuIleLeuLysTyrProPheArgGlu   130
          |||||||| |||||::| |||||||||||||| ::||| |||||||||
Db   181 CTCTTCCTCCACCTGTTTCAGCATCTACGCTGTGTGATCATTCACCAATGAGGTGC   240

Qy   131 HisLeuLeuGlyLysLysGluPheAlaIleLeuIleLeuSerLeuAlaIleTrpValLeuVal   150
          ||| ::: |||||| ||||||||||| ||||||||::::|||||| |||||
Db   241 TTTTCCAATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGGCGTGGATCATTTCA   300

Qy   151 ThrLeuGluLeuGluProIleLeuGluPheIleLeuAsnProValIleThrArgAspAsnGlyThr   170
          ||||||||||||| ||||||||||||| |||||| |||||||| :: |||||
Db   301 CTGGTAGCTGTGTCATTCCGATGACCTTCTTGATCACATCAACAACAGAGACAGATCA   360

Qy   171 ThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCys   190
          ||| ||||||||||||||||::: |||||| |||:::|||||| |||||| ||||
Db   361 GCCTGTCTGCAGCCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTTGTACAACCTGATT   420

Qy   191 LeuPheLeuThrPheLeuLeuProLeuLeuPheValMetCysPhePheTyrTyrLysIle   210
          ||||||:::|| ||||||| ||||||||||||::: ||||||||||||||
Db   421 TTGACTGCAACTACTTTCTGCCCTCCCCTTGGTGATAGGGTACACTTTGCTATACCCAGGATT   480

Qy   211 AlaLeuPheLeuGlyLysGlnArgAsnArgGlnValAlaAlaThrAlaLeuProLeuGlyLysPro   230
          ||| ||||||::::||||||||||||||||||||||||| |:::
Db   481 ---ATCCACACTGTCACCATGGACGTGCAAACTGACAGCTGCCTTAAG---CAGAAAGCA   534

Qy   231 LeuAsnLeuValIleLeuMetAlaValValAlaIlePheSerValProPheThrProTyrHisVal   250
          ||| ||:::|||||||::: |||||| ::: ||||::: :::
Db   535 CGAAGGCTAACCATTCTCGCTACTCCCTTGCATTTACGTTTTTTACCCTTCCATATC   594

Qy   251 MetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThr---   269
          :::||:::|| |||||| ||||||||||||||||||::: ||||||
Db   595 TTCAGGGTCATTGGATCGGAAATCTCGGCCTGCTTTCA------CAGAAAGCA   645

Qy   270 GlnValValIleLeuAsnSerPheTyrIleValThrArgProLeuAlaPheLeuAsnAsnSerVal   289
          ::: ||||||||||:::||||||||||||||||||||||||||:::
Db   646 GAGAATCAGATCCATGAAGCTTACATCGTTTCAGCCATTAGCTGCTCTGAACACCTTT   705

Qy   286 LeuAsnSerValIleAsnProValPheTyrPheLeuGlyAspHisPheArgAspMet   305
          |||||||::: ::: |||||||||||||||||||||||||||||||:::
Db   706 GGTAACCTGTTACTATATGTGGGTGGGTCAGCGACGAACTTTCAGCGAGGTGTCTGCTCAACA   765

Qy   306 LeuMetAsnGlnLeuArg   311
          ::: |:::
Db   766 CCCTTCCATARCTTGAGGGTCATTGGATCGAAATCTCGCCTGCTTTCA------ATC   816

Qy   310 LeuArg   311
          :::|||
Db   706 GGTAACCTGTTACTATATGTGGGTGGGTCAGCGACGAACTTTCAGCGAGGTGTCTGCTCAACA   765

US-09-943-798-1
Sequence 1, Application US/09943798
Patent No. US20020065215A1
GENERAL INFORMATION:
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Polypeptide
FILE REFERENCE: QG1021
CURRENT APPLICATION NUMBER: US/09/943,798

RESULT 2
US-09-943-798-1

Db   766 GTGAGA 771

RESULT 3
US-09-826-791-1

; Sequence 1, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
;   APPLICANT: Pfizer Inc
;   TITLE OF INVENTION: No. US20010039037A1el Polypeptide
;   FILE REFERENCE: PC10914ADAM
;   CURRENT APPLICATION NUMBER: US/09/826,791
;   CURRENT FILING DATE: 2001-04-05
;   PRIOR APPLICATION NUMBER: 0008504.3
;   PRIOR FILING DATE: 2000-04-05
;   PRIOR APPLICATION NUMBER: 60/198,367
;   PRIOR FILING DATE: 2000-04-19
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 1
;   LENGTH: 993
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-826-791-1

Alignment Scores:
Pred. No.:

Score:	1.52e-31
Percent Similarity:	384.00
Best Local Similarity:	47.928
Query Match:	30.36%
	21.98%
	10

Length:	993
Matches:	102
Conservative:	59
Mismatches:	125
Indels:	50
Gaps:	11

US-09-765-034-2 (1-334) x US-09-826-791-1 (1-993)

Qy   8 AsnAlaThrCysLysAsnTrpLeuAlaIleAlaGluAlaAlaLeuGluLysTyr---------- 24
            ||| ||| ::|||| ::
Db   10 AATGGCACCTTCAGCAATAACAACACGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA 69

Qy   25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
            ||||||||||||||||||| ::||||| |||||||||| :
Db   70 TTTTTTCCCAATTGTATATCTGATAATATTTTTCTGGGAGTCTTGGGAAATGGGTTGTCC 129

Qy   45 ValTyrGlyTyrIlePheSerLeuLysAsnThrProAsnSerSerAsnIleTyrLeuPheAsn 64
            ||| ::|||| || ::||::::||
Db   130 ATATATAGTTTTCCTCCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTCATGCTAAAT 189

Qy   65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrArgAla 84
            ||| |||::|||||||||| ||||||| |
Db   190 CTGGCCAATTCAGATCAGTCCTGTTCATAAGCACGCTTCCCTTCAGGCGTCGACTATATCT 249

Qy   85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerGluAsnArgTyrValLeuHis 103
            ||| || :: ||| |||||||::||
Db   250 AGAGGCTTCCAATTGGAATATTTGGAGACCTGGCCTGCAGGATTATGTGTCTTAATTCCTTGTAT 309

Qy   104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIle 123
            ||| || |||: :|||| ||:|::|||
Db   310 GTCACACATGTACAGCAGTATTTTATTTCCTGACCGTGCTGTTGCGTTTCCTGGCA 369

Qy   124 IleLysTyrProPheArg---GluHisLeuLeuGlnLysLysGluPheAlaIleLeuIle 142
            ||| ::||||||||| :||||||
Db   370 ATGGTCACCCCTTCGCTTCGCATGTCACCAGCAGTGCCTGGAATCCTCTGT 429

Qy   143 SerLeuAlaIleTrpAlaValThrLeuGluLeuLeuProIleLeuProLeuIleAsn 162
            ||| || ||| |||||::
Db   430 GGGATC---ATATGGAATCCTTATCATCGGCTTCCTCAATAATCCTCCTG------ 474

Qy   163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182
            ||| || |||||||::
Db   475 ------------GACAGTGGCTCTGAGCAGAACGGCAGTGCACATCA------ 510

Qy   183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu---------------- 193
            ||| ||| |||
Db   511 --------------------TGCTTGAGCTGAAATCTCTATAAAAATTGCTAAGCTGCAG 549

RESULT 4
US-09-828-478-1

; Sequence 1, Application US/09828478
; Patent No. US20020015528A1
; GENERAL INFORMATION:
;   APPLICANT: Xiao, Yonghong
;   TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
;   TITLE OF INVENTION: Protein
;   FILE REFERENCE: 04974.00458
;   CURRENT APPLICATION NUMBER: US/09/828,478
;   CURRENT FILING DATE: 2001-04-09
;   PRIOR APPLICATION NUMBER: 60/195,196
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: 60/254,876
;   PRIOR FILING DATE: 2000-12-13
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 1
;   LENGTH: 1041
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-828-478-1

Alignment Scores:
Pred. No.:

Score:	1.62e-31
Percent Similarity:	384.00
Best Local Similarity:	47.92%
Query Match:	30.36%
	21.98%
	9

Length:	1041
Matches:	102
Conservative:	59
Mismatches:	125
Indels:	50
Gaps:	11

US-09-765-034-2 (1-334) x US-09-828-478-1 (1-1041)

Qy   8 AsnAlaThrCysLysAsnTrpLeuAlaIleAlaGluAlaAlaLeuGluLysTyr---------- 24
            ||| ||| ::|||| ::
Db   8 AATGGCACCTTCAGCAATAACAACACGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA 117

Qy   25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
            ||||||||||||||||||| ::||||| |||||||||| :
Db   58 TTTTTTCCCAATTGTATATCTGATAATATTTTTTCTGGGAGTCTTGGGAAATGGGTTGTCC 177

Qy   45 ValTyrGlyTyrIlePheSerLeuLysAsnThrProAsnSerSerAsnIleTyrLeuPheAsn 64
            ||| ::|||| || ::||:::::||
Db   118 ATATATAGTTTTCCTCCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTCATGCTAAAT 237

Qy   194 ----------------LeuGlyPheLeuIleProLeuPheValMetCysPhe 205
            ::|||| |||::||||| ||| ::
Db   550 ACCATGAACTATATTGCCTTGGTGGGCTTGGGCGTGCCTGCTGCCATTTTTGCACACTGCATC 609

Qy   206 PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAla 224
            ||| ||| ||||||||||||| :
Db   610 TGTTATCTGCTGATCATTCCGGGTTCTGTTAAAAGTGGAGTCCCAGAAATCGGGGCTGGG 669

Qy   225 LeuProLeuGluGlyLysProLeuAsnLeuValIleMetAlaValValIlePheSerValPro 244
            ::||| ||| :::::||| ::|||
Db   670 GTTTCTCACAGGAAGGCAGCTGACCACCATCACTCACCTTGAATCACTTCTCTTGGT 729

Qy   245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
            ||| ||| |||:::||| :
Db   730 TTCCTGCCCTATCACACACTGAGGACCGTC--------------- 777

Qy   265 GlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThrArgProLeuAla 284
            ||| || :::|||||||||
Db   778 GTGGGTTTATGCAAAGAC---AGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCA 834

Qy   285 PheLeuAsnSerValIleAsnProValPheThrTyrPheLeuLeuGlyAspHisPheArgAsp 304
            ||| ::: |||:::||||||
Db   835 GCAGCCAATGCCCTGCTTCACATCCTCTGCTCTATTACTTTGCTCGGGGGAGAATTTAAGGAC 894

Qy   305 MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr 318
            ||| ::: |||:::||||
Db   895 AGACTAAAGTCTGCACTCAGAAAGCCATCCACAGAAGGCAAAGACA 942

Qy   65 LeuSerValSerAspLeuValThrLeuProMetLeuIleArgSerTyrArgAla 84
         |||:||:||||:|||||||:|||||:|||:|||||||||
Db   238 CTGGCCAGTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTACTATTCTT 297

Qy   85 AsnGly----AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103
         |||: ||||:||::|||||::||||||
Db   298 AGAGGCTCCAATTGGATATATTTGGAGACCTGGCCTGCCAGGATTATGTCTTATTCCTTGTAT 357

Qy   104 AlaAsnLeuUtyrThrSerIleLeuPheLeuGluThrPheIleLeuSerIleLeuAspArgTyrLeuIle 123
         |||::|||||:||||||||||:|||||::||||||
Db   358 GTCAACAATCTGTACACCAGTATTTTATTTCTGACCTGTGTTGCGTTTCGTGGCA 417

Qy   124 IleLysTyrProPheArg---GluHisLeuLeuGlnLysGlyGluPheAlaIleLeuIle 142
         |||::: ||||::||||
Db   418 ATGGTTCACCCCTTTCGGCTTCGCATGTCACCACATCAGGAGTGCCTGGATCCTCTGT 477

Qy   143 SerLeuAlaIleTrpLeuValThrLeuGluLeuProIleLeuLeuAsn 162
         ||::|||||::||||:|||||
Db   478 GGGATC--ATATGGAATCCTTATCATGGCTTCCCCAATAATGCTCCTG--- 522

Qy   163 ProValIleThrAspAsnGlyThrThrCysSerAsnAspPheLeuSerSerGlyAspProAsn 182
         ||||::||||||:::|||
Db   523 ------GACAGTGGCTCGAGCAGAACGCAGTGCACATCA------ 558

Qy   183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu--- 193
         :||
Db   559 -------------TGCTTAGACGTGAATCTCTTATAAAATTGGTCAAGCTGCAG 597

Qy   194 -------LeuGlyPheLeuIleProLeuPheValMetCysPhe 205
         :::|||||||||:::
Db   598 ACCATGAACTATATTGCCTTGGGTGGGGCTGCCTGCCTGTACTCAGCATC 657

Qy   206 PheThrTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaIleThrAla 224
         ||| :::|||
Db   658 TGTTATCTGCTGATCAATTCGGGTTCTGTTGTTAAAAGTGGAGAGTCCCCAGAATCGGGGGTCGCG 717

Qy   225 LeuProLeuGluLysProLeuAsnLeuValIleIleMetAlaValValIlePheSerValPro 244
         ||| :::|||||:::||||
Db   718 GTTTCTCACGAGGAGGCACTCACCACCATCAATCACCTTGATCATCTTCTTCGTGT 777

Qy   245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
         ||| ::|||||||||||:::|||
Db   778 TTCCTGCCCTATCACACACTGAGGACCGTC---CACTGACGACATGGAAA 825

Qy   265 GlnTyrTyrGlnTyrThrGlnValValLeuAsnSerPheTyrIleValThrArgProLeuAla 284
         ||| :::||||||||
Db   826 GTGGGGTTATGCAAAGAC---AGACTGCATAAAAGCTTTGGTTATCACACTGGCCCTTGGCA 882

Qy   285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp 304
         |||:||| :::||||||||
Db   883 GCACCCAATGCCTGCTTCAATCCTCTGCTCTATTACTTTCCTGGGAGAATTTTAAGGAC 942

Qy   305 MetLeuMetAsnGlnLeuArg------HisAsnPheLysSerLeuThr 318
         ||| :||
Db   943 AGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCAAAGACA 990

; SEQ ID NO 5
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION:(1)..(1041)
US-09-826-791-5

US-09-765-034-2 (1-334) x US-09-826-791-5 (1-1041)

Alignment Scores:
Pred. NO.:
Score: 1.62e-31
                        384.00   Length: 1041
Percent Similarity: 47.92%   Matches: 102
Best Local Similarity: 30.36%   Conservative: 59
Query Match: 21.98%   Mismatches: 125
DB: 10   Indels: 50
                                                   Gaps: 11

Qy   8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaAlaLeuGlyLysTyr----- 24
         :::||| ::|||
Db   58 AATGGCAACTTCAGCAATAACAACAGCAGGAACTGCAACATTGAAAACTTCAAGAGAGAA 117

Qy   25 TyrLeuSerIlePheTyrTyrGlyTyrIleGluPheValAlaGlyValAlaValLeuGlyAsnThrIleVal 44
         :::|||
Db   58 CTGGCCAGTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTACTATTCTT 117

Qy   45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerAsnIleTyrLeuPheAsn 64
         ||| |||
Db   178 ATATAATGGTTTCCTGCAGCCTTATAAGAAGTCCCACACTCTGAACGTTTCATGCTAAAT 237

Qy   65 LeuSerValSerAspLeuValThrLeuProMetLeuIleArgSerTyrArgAla 84
         |||:||:||||:|||||||:|||||:
Db   238 CTGGCCAGTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTACTATTCTT 297

Qy   85 AsnGly----AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103
         |||:
Db   298 AGAGGCTCCAATTGGATATATTTGGAGACCTGGCCTGCCAGGATTATGTCTTATTCCTTGTAT 357

Qy   104 AlaAsnLeuUtyrThrSerIleLeuPheLeuGluThrPheIleLeuSerIleLeuAspArgTyrLeuIle 123
         |||::|||||:||||||||||:
Db   358 GTCAACAATCTGTACACCAGTATTTTATTTCTGACCTGTGTTGCGTTTCGTGGCA 417

Qy   124 IleLysTyrProPheArg---GluHisLeuLeuGlnLysGlyGluPheAlaIleLeuIle 142
         |||:::
Db   418 ATGGTTCACCCCTTTCGGCTTCGCATGTCACCACATCAGGAGTGCCTGGATCCTCTGT 477

Qy   143 SerLeuAlaIleTrpLeuValThrLeuGluLeuProIleLeuLeuAsn 162
         ||::|||||::||||:|||||
Db   478 GGGATC--ATATGGAATCCTTATCATGGCTTCCCCAATAATGCTCCTG--- 522

Qy   163 ProValIleThrAspAsnGlyThrThrCysSerAsnAspPheLeuSerSerGlyAspProAsn 182
         ||||::||||||:::|||
Db   523 ------GACAGTGGCTCGAGCAGAACGCAGTGCACATCA------ 558

Qy   183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu--- 193
         :||
Db   559 -------------TGCTTAGACGTGAATCTCTTATAAAATTGGTCAAGCTGCAG 597

Qy   194 -------LeuGlyPheLeuIleProLeuPheValMetCysPhe 205
         :::|||||||||:::
Db   598 ACCATGAACTATATTGCCTTGGGTGGGGCTGCCTGCCTGTACTCAGCATC 657

Qy   206 PheThrTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaIleThrAla 224
         ||| :::|||
Db   658 TGTTATCTGCTGATCAATTCGGGTTCTGTTGTTAAAAGTGGAGAGTCCCCAGAATCGGGGGTCGCG 717

Qy   225 LeuProLeuGluLysProLeuAsnLeuValIleIleMetAlaValValIlePheSerValPro 244
         ||| :::||||||:::||||
Db   718 GTTTCTCACGAGGAGGCACTCACCACCATCAATCACCTTGATCATCTTCTTCGTGT 777

Qy   245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
         ||| ::||||||||||:::|||
Db   778 TTCCTGCCCTATCACACACTGAGGACCGTC---CACTGACGACATGGAAA 825

RESULT 5
US-09-826-791-5
Sequence 5, Application US/09826791
Patent No. US20010039037A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
TITLE OF INVENTION: No. US20010039037A1e1 Polypeptide
FILE REFERENCE: PCI0914ADAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0

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Db   778  TTCCTGCCTATCACACACTGAGGACGGTC------------CACTTGACGACATGGAA  825
Qy   265  GlnTyrGlnCysThrGlnValValIleValThrArgProLeuAla  284
Db   826  GTGGGTTTATGCAAAGAC---AGACTGCCATAAAGCTTTGGTTTATCACACTGCCC  882
Qy   285  PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp  304
Db   883  GCAGCCAATGCCTGCTTCAATCCTCTGCTCTTATTACTTTGCTGGGGAGAATTTTAAGGAC  942
Qy   305  MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr  318
Db   943  AGACTAAAGTCTGCACTCAGAGAAAAGGCCATCCACAGAGAGGCAAAGACA  990
```

RESULT 6
US-09-866-230-6
Sequence 6, Application US/09866230
Patent No. US20020150901A1
GENERAL INFORMATION:
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: No. US20020150901A1e1 Nucleic Acids, Polypeptides, Methods of Mak...
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1041)

Alignment Scores:
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Pred. No.:                 10
Score:              1.62e-31
                      384.00
Percent Similarity:   47.92%        Length:        1041
Best Local Similarity: 30.36%       Matches:        102
Query Match:          21.98%        Conservative:    59
DB: US-09-866-230-6                 Mismatches:     125
                                    Indels:          50
                                    Gaps:            11
```

US-09-765-034-2 (1-334) x US-09-866-230-6 (1-1041)

```
Qy     8  AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaLeuGluLysTyr--------   24
Db    58  AATGGCACCTTGCAATAACACAGGAACTGCACAATTGAAAAACTTCAAGAGAA  117

Qy    25  TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyValLeuGlyAsnThrIleVal   44
Db   118  TTTTTCCCAATTGTAATATCTGATAAATATATTTTTCTGGGGAGTCTTGGAAATGGGTTGTCC  177

Qy    45  ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerAsnIleTyrLeuPheAsn   64
Db   178  ATATATGTTTTGCTCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAAT  237

Qy    65  LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla   84
Db   238  CTGGCCAATTCAGATCCCCGTTCATAAGCACGCTTCCCTTCAGGGTCGACTATTACTT  297

Qy    85  AsnGly--AsnTrpIleTyrGlyAspValLeuCysLysIleSerAsnArgTyrValLeuHis  103
Db   298  AGAGGCTCCAATGGATATTTGGAGACCTGCGCAGGATATATGTCTTATTCCTTGTAT  357

Qy   104  AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIle  123
Db   358  GTCAACAATGACAGACAGTATTATTTCCTGACCGTTCATGTGTCGTTTCCTGGCA  417

Qy   124  IleLysTyrProPheArg--GluHisLeuLeuGlnLysLysGluPheAlaIleLeuIle  142
```

RESULT 7
US-09-828-478-3
Sequence 3, Application US/09828478
Patent No. US20020155228A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
FILE REFERENCE: 04974.00058
CURRENT APPLICATION NUMBER: US/09/828,478
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1430
TYPE: DNA
ORGANISM: Homo sapiens
US-09-828-478-3

Alignment Scores:
```
Pred. No.:                  9
Score:              2.54e-31
                      384.00
Percent Similarity:   47.92%        Length:        1430
Best Local Similarity: 30.36%       Matches:        102
Query Match:          21.98%        Conservative:    59
                                    Mismatches:     125
                                    Indels:          50
                                    Gaps:            11
```

```
Db   418  ATGGTTCACCCCTTTCGGCTTCTTGGCATGTCACCAGCATCAGGAGGAGTGCCTGGATCCTCTGT  477
Qy   143  SerLeuAlaIleThrTyrValIleLeuValThrLeuGluLeuGlnLeuLeuProIleLeuIleAsn  162
Db   478  GGGATC---ATATCAGATCCTTATCATGGCTTCCTTCAATAATGCTCCTG------------  522
Qy   163  ProValIleThrAspAsnGlyThrThrCysAsnAspSerPheAlaSerGlyAspAsn  182
Db   523  --------GACAGTGGGGTCTGAGACAGAACGGCAGTGTCACATCA-------  558
Qy   183  TyrAsnLeuIleTyrSerMetCysLeuThrLeu-------  193
Db   559  --------TGCTTAGAGCTGAATCTCTATAAAAATTGCTAAGCTGAG  597
Qy   194  ------------------------LeuGlyPheLeuIleProLeuPheValMetCysPhe  205
Db   598  ACCATGAACTATATTGCCTTGGTGTGGGCTGCCTGCTCCCATTTTTCACACTGCAC  657
Qy   206  PheTyrTyrLys---IleAlaLeuPheLeuLeuLysGlnArgAsnArgGlnValAlaIleThrAla  224
Db   658  TGTTATCTGCTGATCATCTCGGGTTCGTTGTTAAAAGTGGAGTCCCAGAATCGGGGCTGCGG  717
Qy   225  LeuProLeuGluGlyLysProLeuAsnLeuValAlaIleIleMetAlaValValAlaValIlePheSerValPro  244
Db   718  GTTTCTCACAGGAGGCAGCTGACCACCATCATCAACCTTGATCATCTTCTCTGTGT  777
Qy   245  PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgArgLeuGlySerTrpLys  264
Db   778  TTCCTGCCTATCACACACTGAGGACGGTC------------CACTTGACGACATGGAA  825
Qy   265  GlnTyrGlnCysThrGlnValValIleValThrArgProLeuAla  284
Db   826  GTGGGTTTATGCAAAGAC---AGACTGCCATAAAGCTTTGGTTTATCACACTGCCC  882
Qy   285  PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp  304
Db   883  GCAGCCAATGCCTGCTTCAATCCTCTGCTCTTATTACTTTGCTGGGGAGAATTTTAAGGAC  942
Qy   305  MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr  318
Db   943  AGACTAAAGTCTGCACTCAGAGAAAAGGCCATCCACAGAGAGGCAAAGACA  990
```

US-09-765-034-2 (1-334) x US-09-828-478-3 (1-1430)

```
Qy      8  AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr---------  24
              |||  |||                         ::|||  ::
Db    310  AATGGCACCTTCAGCAATAACACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA  369

Qy     25  TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal  44
              |||   :::||||||||||||||||||||||||||||||||||||||      :::
Db    370  TTTTTCCCAATTGTATATCTGATAATATATTTTTCTGGGGAGTCTTGGGAAATGGGTGTCC  429

Qy     45  ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn  64
              |||                  ::|||:|||||||:::
Db    430  ATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTCATGCTAAAT  489

Qy     65  LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla  84
              |||:::|||||||||||||||||   ::|||||||:::||||||||
Db    490  CTGGCCAATTCAGATCTCCGTTCATAACAGCCTTCAGGGCTGACTATATCTT  549

Qy     85  AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerSerAsnArgTyrValLeuHis  103
              |||                ::|||||:|||            :::
Db    550  AGAGGCTCCAATTGGATATATTTGGAGACCTGCCCTGCAGGATTATGTCTTAATTCCTTGTAT  609

Qy    104  AlaAsnLeuTyrThrSerIleLeuGluPheLeuThrPheIleSerIleLeuAspArgTyrLeuIle  123
              |||||:::||||||                      :::
Db    610  GTCAACATGTACAGCAGTAGTAATTTATTTCCTGACCGTTGCGTTTCCTGGCA  669

Qy    124  IleLysTyrProPheArg---GluHisLeuLeuGlnLysLysGlyGluPheAlaIleLeuIle  142
              ||| :::||||||||||        ||:::
Db    670  ATGGTTCACCCCTTTCGGCTTCTGCAATGTCACCAGCATCAGGAGTGCCTGGAATCCTCTGT  729

Qy    143  SerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuLeuAsn  162
              :::        |||||::|||||:::||||||||
Db    730  GGGGATC---ATATGGATCCTTATCATGGGCTTCCTCAATAATGCTCTG  774

Qy    163  ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn  182
              |||           :::||||||||::|||
Db    775  GACAGTGGCTCTGACGACAACGGCAGTGTCACATCA  810

Qy    183  TyrAsnLeuIleTyrSerMetCysLeuThrLeu---------  193
              ||||||  |||
Db    811  ------------TGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAG  849

Qy    194  -----------LeuGlyPheLeuIleProLeuPheValMetCysPhe  205
                   |||::|||||||||||||
Db    850  ACCAGTAACTATATTGCCCTTGGTGGTGGGGTGCCTGCCTGCCATTTTTCACACTCAGCATC  909

Qy    206  PheTyrTyrLys---IleAlaLeuPheLeuGlyAsnArgGlnValAlaThrAla  224
              |||   :::            :::|||
Db    910  TGTTAACTTGCTGATCATTCCGGTTCGTTAAAAGTGGAGGTCCCAGAATCGGGGTGCCGG  969

Qy    225  LeuProLeuGluGlySerProLeuAsnLeuValIleMetAlaValIleIlePheSerValPro  244
              :::|||   |||||||||||||||   :::
Db    970  GTTTCCTCAGAGAGGCACTGACCAACCATCATCATCATCGATCATCTTTCTTGTGT  1029

Qy    245  PheThrProThrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys  264
              |||||||||||||||   :::||||||
Db   1030  TTCCTGCCCTATCACACACTGAGGACCGTC---CACTTGACGACATGGAAA  1077

Qy    265  GlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThrArgProLeuAla  284
              |||          ---AGACTGCAATAAAAGCTTTGGTTATCACACTGGCCTTGGCA  1134
Db   1078  GTGGGGTTTATCAAAGAC---AGACTGCAATAAAAGCTTTGGTTATCACACTGGCCTTGGCA  1134

Qy    285  PheLeuAsnSerValIleLeuAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp  304
              |||||||||||||||||||||||::|||||::||||||||
Db   1135  GCAGCCAATGCCTGGCTTCAATCCTCTGCTCTATTACTTGCTGGGGAGAATTTTAAGGAC  1194

Qy    305  MetLeuMetAsnGlnLeuArg------HisAsnPheLysSerLeuThr  318
              |||    :::|||                ||||||
Db   1195  AGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCCAAGACA  1242
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RESULT 8
; US-09-728-952-26
; Sequence 26, Application US/09728952

```
Alignment Scores:
Pred. No.:                                    Length:       1700
Score:            3.25e-31                     Matches:      102
Percent Similarity:  47.92%                    Conservative: 59
Best Local Similarity: 30.36%                  Mismatches:   125
Query Match:      21.98%                        Indels:       50
DB:               10                            Gaps:         11
```

US-09-765-034-2 (1-334) x US-09-728-952-26 (1-1700)

```
Qy      8  AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr---------  24
              |||  |||                         ::|||  ::
Db    289  AATGGCACCTTCAGCAATAACACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA  348

Qy     25  TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal  44
              |||   :::||||||||||||||||||||||||||||||||||||||      :::
Db    349  TTTTTCCCAATTGTATATCTGATAATATATTTTTCTGGGGAGTCTTGGGAAATGGGTGTCC  408

Qy     45  ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn  64
              |||                  ::|||:|||||||:::
Db    409  ATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTCATGCTAAAT  468

Qy     65  LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla  84
              |||:::|||||||||||||||||   ::|||||||:::||||||||
Db    469  CTGGCCAATTCAGATCTCCGTTCATAACAGCCTTCAGGGCTGACTATATCTT  528

Qy     85  AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerSerAsnArgTyrValLeuHis  103
              |||                ::|||||:|||            :::
Db    529  AGAGGCTCCAATTGGATATATTTGGAGACCTGCCCTGCAGGATTATGTCTTAATTCCTTGTAT  588

Qy    104  AlaAsnLeuTyrThrSerIleLeuGluPheLeuThrPheIleSerIleLeuAspArgTyrLeuIle  123
              |||||:::||||||                      :::
Db    589  GTCAACATGTACAGCAGTAGTAATTTATTTCCTGACCGTTGCGTTTCCTGGCA  648

Qy    124  IleLysTyrProPheArg---GluHisLeuLeuGlnLysLysGlyGluPheAlaIleLeuIle  142
              ||| :::||||||||||        ||:::
Db    649  ATGGTTCACCCCTTTCGGCTTCTGCAATGTCACCAGCATCAGGAGTGCCTGGAATCCTCTGT  708

Qy    143  SerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuLeuAsn  162
              :::        |||||::|||||:::||||||||
Db    709  GGGGATC---ATATGGATCCTTATCATGGGCTTCCTCAATAATGCTCTG------  753
```

```
Qy    163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182
          |||::|||||:|||           ||           ::|||
Db    754 --------------GACAGTGGCGCTCTGAGCAGAACGGCAGTGTGCACATCA-------- 789

Qy    183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu-------------------------- 193
          |||||
Db    790 -----------TGCTTAGAGCTGAATCTCTATAAAAATTGCTAAGCTGCAG--------- 828

Qy    194 ----------------LeuGlyPheLeuIleProLeuProPheValMetCysPhe 205
                          ::|||||       ||||||   ||    :::
Db    829 ACCATGAACTATATTGCCTTGGTGGGTGGCCTGCCCATTTTCACACTTCAGCATC 888

Qy    206 PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAla 224
          |||       :::                     |||||  :::||||||||
Db    889 TGTTTATCTGCTGATCATTCGGGGTTCTGTTAAAAGTGGAGGTCCCAGAAATCGGGGCG 948

Qy    225 LeuProLeuGlyLysProLeuAsnLeuValIleMetAlaValAlaValIlePheSerValPro 244
          |||||||   ||||   |||                    ||:::
Db    949 GTTTCTCACAGGAAGGGACACTGACCACCATCACCATCATGCAGAATTTCTTCTTTGTGT 1008

Qy    245 PheThrProThrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
          |||||||||||||||        |::|||||||||||||||::|||
Db   1009 TTCCTGCCTATCACACACTGAGGACGCGTC------------CACTTGACGACATGGAA 1056

Qy    265 GlnTyrGlnCysThrGlnValValIleLeuAsnSerPheTyrIleValThrArgProLeuAla 284
          ||||||:::||||                    ||||||
Db   1057 GTGGGGTTTATGCAAAGAC--AGACTGCCATAAAGCTTTGGTTATCACACTGCGCCTTGGCA 1113

Qy    285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp 304
          ||        :::                  |||||||||||   :::|||
Db   1114 GCAGCCAATGCCTGCTTCAAATCCTCTGCTCTATTACTTGCTCGGGGAGAATTTTAAGGAC 1173

Qy    305 MetLeuMetAsnGlnIleuArg--------HisAsnPheLysSerLeuThr 318
          |||    |||||||                |||
Db   1174 AGACTAAAGTCTCCACTCCAGAAAAGGCCATCCACAGAAGAGGCAAAGACA 1221
```

Score: 346.50   Matches: 84
Percent Similarity: 52.56%   Conservative: 39
Best Local Similarity: 35.90%   Mismatches: 85
Query Match: 19.838   Indels: 26
DB: 10   Gaps: 5

US-09-765-034-2 (1-334) x US-09-728-422-1 (1-1313)

```
Qy      8 AsnAlaThrCysLysAsnTrpLeuAlaAlaLeuAlaAlaLeuGluAlaLeuGluLysTyrTyrLeuSer 27
          :::|||||       ||      ||:::                |||||||
Db    613 AATTGCACTGATGAAAAC---------------ATCCCACTCAAGATGCGACTACCTCCCT 657

Qy     28 IleGluPheTyrGlyIleLeuGluPheValAlaGlyValValLeuGlyValAsnThrIleValValTyrGly 47
          ::: ||||||||||        |||||||       |||||::||||||
Db    658 GTTATTTAGGCATTATATCTTCCCTCGTGGGATTCCAGGAAATTCCAGGTAGTAGTANCCACT 717

Qy     48 TyrIleProSerLeuLysAsnTrpAsnSerSerAsnIleThrLeuPheAsnLeuSerVal 67
          |||||||||       ||      ::: |||||||            |||::|||
Db    718 TACATTTTCAAAAATGAAGACCTTGGAAGAGCGACCACCATCAATTATGCCCAGTGCCTGC 777

Qy     68 SerAspLeuAlaPheLeuCysThrIleLeuProMetLeuIleLeuArgSerTyrAlaAsnGly-- 86
          |||||||||::|||||              |||||||||||       :::|||
Db    778 ACAGANCTCGCTGTATCTGACCAGCCTCCCTCCTTGTTCAGCATTCCTCACTGTGTGGATCAGTCAC 837

Qy     87 AsnIleProIleLeuTyrGlyValLeuCysIleSerSerAsnArgTyrValLeuHisAlaAsnLeu 106
          |||||||||||||||||||        ::: |||           |||||||
Db    838 AACTGGATCTTTGGAGATTTCACTGTAGTTTNATCCGCTTCAGCTTCCATTCAACCTG 897

Qy    107 TyrThrSerIleLeuPheLeuThrPheIleLeuAspArgArgTyrLeuIleIleLeuLysTyr 126
          |||||||||::||||||||||||||||         :::|||||   |||::|||
Db    898 TATAGCAGCATCCTCTTCCTCCACCTGTTCAGCATCTTCCGGCTACTGTGTGGATCAGTCAC 957

Qy    127 ProPheArgGluHisLeuLeuGlnLysGluPheAlaIleLeuLeuSerLeuAlaIle 146
          |||||||||           |||            :::|||
Db    958 CCAATGAGCTGCTTTTCCATTCACAAAACTGATGTGCAGTTGTTAGCCTGTGCTGGTG 1017

Qy    147 TrpValLeuValThrLeuGluLeuLeuProLeuLeuAsnProValIleThr 166
          ::: ||||||       |||            ||||||
Db   1018 TGGATCATTTCACTGTAGCCTGTCAATTCCGATGGACCTTCTTGACACATCAACCAACACAG 1077

Qy    167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn-------- 182
          |||           :::              |||   |||
Db   1078 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAGAACTCAAATACTATTAAGTGG 1137

Qy    183 TyrAsnLeuIleTyrSer-MetCysLeuThrLeuGluGlyPheLeuIleProLeuProPheVal 202
          |||||:::              |||
Db   1138 TACAACCTAATTTTGACTCGCAAACTACTTTGCCTC-----------CCCTTGGTGAT 1182

Qy    202 IleMetCysPhePheTyrTyrTyrLysIleAla------- 212
          ||||            |||
Db   1183 AGTGACACTTTGCTATACCACAGGATTATCCACACTCTGACCACCATGGACTGCCAAACTGACAG 1242

Qy    212 uPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeu 225
          |||||||||||||       |||:::
Db   1243 CTGCCTTAAGCAGAAAGCACGGAAGCCTAACCATTCTGCTA 1282
```

RESULT 10
US-09-788-133-1
Sequence 1, Application US/09788133
Patent No. US20020052001A1
GENERAL INFORMATION:
  APPLICANT: GLAXO GROUP LTD
  TITLE OF INVENTION: ASSAY
  FILE REFERENCE: P79011
  CURRENT APPLICATION NUMBER: US/09/788,133
  CURRENT FILING DATE: 2001-02-20
  NUMBER OF SEQ ID NOS: 2
  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
  LENGTH: 1020
  TYPE: DNA
  ORGANISM: homo sapiens
  FEATURE:

Alignment Scores: 2.01e-27   Length: 1313
Pred. No.:   1313

```
;
; NAME/KEY: CDS
US-09-788-133-1    LOCATION: (1)..(1020)
DB:

Alignment Scores:
Pred. No.:
Score:                    1.1e-26
Percent Similarity:       338.00
Best Local Similarity:    48.85%
Query Match:              27.54%
DB:                       19.35%
                          10

Length:          1020
Matches:         84
Conservative:    65
Mismatches:      126
Indels:          30
Gaps:            6

US-09-765-034-2 (1-334) x US-09-788-133-1 (1-1020)

Qy      18 GluAlaAlaLeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGly 37
           ||||                      :::       |||||| :::|||:|||:||||
Db      76 GAGACGGCCACTGGAGAACATGCTGTTCGCGCTCCTTACCTTCTGGAATTTATCCTGGCT 135

Qy      38 ValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLeuLysAsnTrpAsnSer 57
           ::|||||||||:|||:::          |||||      :::       |||
Db     136 TTAGTTGGCAATACCCTGGTCTGTGGCTTTTCATCCGAGACCACAAGTCCGGACCCCG 195

Qy      58 SerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuPro 77
           ::|||:|||:||   ||||        ||||| :::|||      |||
Db     196 GCCAACGTGTTCCTGAtGCATCTGGCCGTGCCGACTTGTGTGCGTGCTTGTTCCTGCC 255

Qy      78 --MetLeuIleArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIle 96
            :::::|||                  |||||:|||||:::      |||
Db     256 ACCCGCCTGGTCTACCACTTCTCTGGGAACCACTGCCCATTGGGGAAATCGCACTGCCGT 315

Qy      97 SerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuLeuPheLeuThrPheIle 116
           |||:::                |||:::|||:|||||||||||||||||||||
Db     316 CTCACGCGGTTCCTCTTCTACCTCAACATGTACGCCAGCAtCTACTTCCTCACCTCGCATC 375

Qy     117 SerIleAspArgTyrTyrLeuIleIleLeuTyrProPheArgGluHisLeuLeuGlnLysLys 136
           |||                 |||:::|||||| :::      :::|||
Db     376 AGCGCCGACACCGTTTCCTGGCCATTGTACCCGGTCAAGTCCCTCAAGCTCCAGGCCCC 435

Qy     137 GluPheAlaIleLeuSerLeuAlaIleLeuTrpValLeuValThrLeuGluLeuLeuPro 156
           ::|||                 |||||||||||:|||      |||
Db     436 CTCTACGCACACTGCGCCTGTGCCTTCCTCGTGGGGTGGGTGACGCTGGAGCTGCTCCCG 495

Qy     157 IleLeuProLeuIleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAla 176
           :::|||                |||:::      |||
Db     496 CTTGCTGGTGAGCCCAGAGACGGTGGCTCTCCTGCCCGAGCGTGTAC 555

Qy     177 SerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPhe 196
           :::      :::||||||                 |||
Db     556 CGGGAGAAGGCCTCCACCATGCCCTGGTG-------     TCCCTGGCAGTGGCCTTC 603

Qy     197 LeuIleLeuProLeuPheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGln 216
           |||                 |||:::|||      :::|||
Db     604 ACCTTCCGTTCATCACCACGGTCACCTGCTTACCTGCTGGCAG 663

Qy     217 ArgAsnArgGlnValAlaThrAlaLeuProLeuGlnLysProLeu---------------- 231
                                 ||| :::|||||||||||
Db     664 --------     GGCCTGCGTGGAGAAGCGCCCTCAAGACAAGGCAGTG 702

Qy     232 AsnLeuValIleMetAlaValValLeuPheSerValProPheThrProTyrHisValMet 251
           :::::::|||                 |||
Db     703 CGCATGAtCGCCATAGTGCCCACTTCCTGGGTCTGCTTCGTGCCTACCACGTCAAC 762

Qy     252 ArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGln------------- 267
           |||:::|||                 :::
Db     763 CGCTCCGTTCTACGTGCTG-----     CACTACCGCAGCCATGGGGCC 801

Qy     268 ------CysThrGlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
                 :::|||                ||||||
Db     802 TCCTGCGCCACCAGCGCATCCTGGCCCCTGCAAACCCATCACCTTCCTGCCTACCAGC 861

Qy     286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
           |||||||                |||   :::      ||||||
Db     862 CTCAACGGGGCCACTGACCCCATCANGTATTTCTTCGTGGCTAGGAGAAGTTCCGCCACGCC 921
```

```
Qy     306 LeuMetAsnGlnLeu 310
           |||   |||   |||
Db     922 CTGTGCAACTTGCTC 936
```

```
Qy     306 LeuMetAsnGlnLeu 310
           |||   |||   |||
Db     922 CTGTGCAACTTGCTC 936
```

```
Pred. No.:
Score:                    1.69e-26      Length:            1068
Percent Similarity:       47.72%        Matches:           88
Best Local Similarity:    26.75%        Conservative:      69
Query Match:              19.26%        Mismatches:        131
DB:                       10            Indels:            41
                                        Gaps:              9

US-09-765-034-2 (1-334) x US-09-864-761-26799 (1-1068)
```

```
Qy    2   LeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaAlaLeu   21
              ||||||||:::::|||:||                                 ||
Db    945 CTGGGAGTTGTTGTTCACTGGGTCTCCCTG------------------------SerAsn   919

Qy    22  GluLysTyrTyrLeuSerIlePheTyrGlyIleGluValValGlyValLeuGlyAsn         41
             |||:||||||:|||::||||||:||:||||                              ||||||
Db    876 GCCATCGTTCATTTGG------------TTCACGGGGTTCAAGTGGAAGACAGTCACACT   826

Qy    42  ThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSer----SerAsn       59
              ||||||||:::::                                          ::|||
Db    918 ------GTTGTATATTGTTGTTGGCTTTTGTTCTGGGAATTCCAGGAAAT                877

Qy    60  IleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeu      79
             |||:|||                                                    :::|||
Db    825 CTGTGGTTCCTCAATCTAGCCATTGCGGATTTCATTTTCTTCCTTTTCTGCCCTGTAC       766

Qy    80  IleLeuArgSerTyrAla---AsnGlyAsnTrpIleTyrGlyValLeuCysIleSerAsn      98
             ||| :::|||                                                    ||
Db    765 ATCTCCTATGGTGCCATCGAAGATTTCCACGGCCCGTTGGCCATCTGCAAAGCCAAT        706

Qy    99  ArgTyrTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIle   118
             ::::|||                                                         ||
Db    705 TCCTTCACTGCCCAGTTGAACATGTTTGCCAGTGTTTTTTTCCTGACAGTGACAGCCCTG      646

Qy    119 AspArgTyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPhe      138
             |||                                                            :::
Db    645 GACCACTATATCATCCACTTGATCATCCGTCTTATCTCATCGGCATCGAACCCTCAAGAAC     586

Qy    139 AlaIleLeuIleSerLeuAlaIleLeuTrpValLeuValThrLeuGluLeuProIleLeu      158
             |||:||||                                                       |||
Db    585 TCTCTGATTGTCATTATATTCATCTGGCTTTGGCTTCTTCTAATTGGGGGTCCTGCCCTG     526

Qy    159 ProLeuIleAsnProValIlePheThrAspAsnGlyThrThrCysAsnAspPheAlaSerSer   178
             |||||||                                                         ||
Db    525 TACTTCCGGGACACTGTGGAGTTCAATAATCACTCTTTGCTATAAACAAATTTTCAGAAG       466

Qy    179 GlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThr----------LeuLeu       194
             ||||||                                          :::||||||
Db    465 CATGATCCTGACCTCACTTTGATCAGGCACCACGATGTCTGACTGGGTGAAAATTTATCATT   406

Qy    195 GlyPheLeuIlePheLeuPheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeu      214
             |||::||||                                                      |||
Db    405 GGCTATCTTCTTCCCTTTGCTAACAAATGAGTATTTGCTAC------TTGTGTCCATCTTC     352

Qy    215 LysGlnArgAsnArgGlnValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuVal      234
             |||||||                                                         ||
Db    351 AAGTGAAGAAGGCAAGCATC------CTGATCTCCAGTAGGCATTTCTGGACAATT          301

Qy    235 IleMetAlaLeuValIlePheSerValProPheThrProTyrHisValMetArgAsnVal      254
             |||||||                                                         ::
Db    300 CTGGTTGTGGTTGTGGGCCTTTGTGGGTTTGGCTCCTTATCACCTGTTTAGCATTTGG       241

Qy    255 ArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsn     274
             |||:||:                                                        ||
Db    240 GAGCTACACCATTCACCACCAAATAGCTATTCCCACCAT------GTCGATGCAG           196

Qy    275 SerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerValIleLeuAsnProValPhe   294
             :::|||                                                          ||
Db    195 GCTGGAATCCCCTCTCCACTGGTTTGGCATTCCTCAACAAGTTGCTTGAACCCCATCCTT     136

Qy    295 TyrPheLeuLeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPhe      314
             ||| |||                                                         |||
Db    135 TAGTCTCATTAAATAAGTAAGAAGTTCCAA------GCTCGCTTCCGGTTCCTCAGTT         88
```

```
Qy    US-09-765-034-2 (1-334) x US-09-864-761-26799 (1-1068)
Db    87   GCTGAGATACTTCAAGTACACACTGTGG   61

Alignment Scores:
Pred. No.:
Score:                    2.54e-26      Length:            1422
Percent Similarity:       47.72%        Matches:           88
Best Local Similarity:    26.75%        Conservative:      69
                                        Mismatches:        131
```

Query Match:
DB:

US-09-765-034-2 (1-334) x US-09-864-761-10158 (1-1422)

	19.26%	Indels:	41
Query Match:		Gaps:	9
DB:	10		

```
Qy     2 LeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeu    21
         ||||||  ||| ::::|||||  || |||
Db  1218 CTGGGAGTTGTTCACTGGGTCTCCCCTG------------------------------ 1192

Qy    22 GluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsn    41
         :::                    |||||  |||::::|||||||
Db  1191 ------------------GTGTTATAATTGTTTGGCTTTTGTTCTGGGAATTCCAGGAAAT 1150

Qy    42 ThrIleValThrTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSer------SerAsn    59
         ||||||||  :::
Db  1149 GCCATCGTCATTTGG------------------TTCACGGCGGTTCAAGTGGAAGAAGACAGTCACCACT 1099

Qy    60 IleTyrLeuPheAsnLeuSerValSerArgAspLeuAlaPheLeuCysThrLeuProMetLeu    79
         ||||:::|||  |||::::||||||  |||
Db  1098 CTGTGGGTTCCTCAATCTAGCCATTGCGGATTTCATTTTTCTTCCTTTCTGGCCCCGTTAC 1039

Qy    80 IleArgSerTyrAla---AsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerSerAsn    98
         |||     |||       ::::|||
Db  1038 ATCTCCTATGTGGCCAAGAAATTCCACTGGCCCTTTGGCATCTGGCTGTGTGCAAAGCCAAT 979

Qy    99 ArgTyrValLeuHisAlaAlaAsnLeuTyrThrSerIleLeuLeuPheLeuThrPheIleSerIle   118
         :::
Db   858 TCTCTGATTGTCATTAATAATTCATCTGGCTTCTTCTCTAAATTGGCGGTTCCTGCCTG 799

Qy   119 AspArgTyrLeuIleIleLeuTyrProPheArgGluHisIleLeuLeuGlnLysLysGluPhe   138
         |||::::|||  |||
Db   918 GACCACTATATCCACTTGATCACGGCACCATGGTCTCTGTCTTATNTCATCACGGGCATCCGAACCCTCAAGAAC 859

Qy   139 AlaIleLeuIleSerLeuAlaIleThrProValLeuValThrLeuGluLeuLeuProIleLeu   158
         |||                    :::
Db   978 TCCTTCACTGCCGGACACTGGAGCGTTCAATAAATCACTCTTGCTATAACAATTTCAGAAG 919

Qy   159 ProLeuIleAsnProValIleThrAspAsnGlyThrThrCysTyrAsnAspPheAlaSerSer   178
         :::
Db   798 TACTTCCGGGACACTGGAGCGTTCAATAAATCACTCTTGCTATAACAATTTCAGAAG 739

Qy   179 GlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThr----------LeuLeu   194
         ||||||                                              :::
Db   738 CATGATCCTGACCTCACTTGATCAGGCACCACCATGGTCTGACTTGGGGTGAAATTTATCATT 679

Qy   195 GlyPheLeuIleProLeuPheValMetCysPhePheTyrTyrPheLysIleAlaLeuPheLeu   214
         ||||||::|||                          |||
Db   678 GGCTACTCTCTTCCCTTTGCTAACAATGAGTATTTGCTAC------TTGTGTCTGTCTTC 625

Qy   215 LysGlnArgAsnArgGlnValAlaIleThrAlaLeuProLeuGlyLysProLeuAsnLeuVal   234
         :::
Db   624 AAGGTGAAGAAGCGAAGCATC------CTGATCTCCAGTAGGCATTTCTGGACAATT 574

Qy   235 IleMetAlaValAlaIlePheSerValProPheThrProTyrHisValMetArgAsnVal   254
         :::::::||  ||||||  |||          :::|||||:::|||||||  :::
Db   573 CTGGTTGTGGTTGCGGCTTTGTGGCTTTGCTGGACTCCTTATCACCTGTTTAGCATTGG 514

Qy   255 ArgIleAlaSerArgLeuGlySerTrpLysSerThrGlnTyrGlnCysThrGlnValValIleAsn   274
         :::
Db   513 GAGCTCACCCATTCACCACACAAAAGCTATTCCCACCAT--------GTGATGCAG 469

Qy   275 SerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPhe   294
         :::
Db   468 GCTGGAATCCCCTCTCCACTGGTTTGGCATTCCTCAAATAGTTGCTTGAACCCATCCTT 409

Qy   295 TyrPheLeuLeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPhe   314
         |||  |||          :::
Db   408 TATGTCCTAAATTAGTTAAGAAGTTCCAA---------------GCTCGCTTCCGGGTCCTCAGTT 361

Qy   315 LysSerLeuThrSerPheSerArgTrp   323
         :::::::      |||
Db   360 GCTGAGATACTCCAAGTACACACTGTGG 334
```

RESULT 13
US-09-104-063-1
; Sequence 1, Application US//09104063
; Patent No. US20020168356A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/104,063
;   FILING DATE: 24-June-1998
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/701265
;   FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/664228
;   FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/076093
;   FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/810782
;   FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B.
;   REGISTRATION NUMBER: 34,659
;   REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-5530
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1933 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear

US-09-104-063-1

Alignment Scores:
Pred. No.:			
Score:	331.00	Length:	1933
	1.49e-25	Matches:	99
Percent Similarity:	45.19%	Conservative:	56
Best Local Similarity:	28.86%	Mismatches:	143
Query Match:	18.95%	Indels:	45
DB:	9	Gaps:	10

US-09-765-034-2 (1-334) x US-09-104-063-1 (1-1933)

```
Qy     7 TrpAsnAlaThrCysLysAsnTrpLeu----------AlaAlaGlu-AlaAlaLeuGl    22
         |||  ::::|||||||||||||||          |||           :::
Db   104 TGGCATGCCACCTGCAAGAATGAGATTACAGCCCCTGTATGCTAGAAACTGAGACACTCAA 163

Qy    22 uLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnTh    42
         |||||| ||| |||            :::||::::||||||||||::
Db   164 CAAGTATGTTGTGATCATCGCCTTATGCCCTAGTGTTCCTGCTGAGCCCTGGGAAAGCTC 223

Qy    42 rIleValThrTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLe    62
         :::          :::|||||||||:::          :::::::||||
Db   360 rIleValThrTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLe    62
```

RESULT 14
US-09-880-261-1

Sequence 1, Application US/09880261
Patent No. US2002004790A1
GENERAL INFORMATION:
APPLICANT: Winnie Chan
APPLICANT: Derk J. Bergsma
APPLICANT: Catherine E. Ellis
TITLE OF INVENTION: A NOVEL G-PROTEIN COUPLED RECEPTOR,
TITLE OF INVENTION: HLTEX11
FILE REFERENCE: AOY1-50025US2

CURRENT APPLICATION NUMBER: US/09/880,261
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/113,933
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 08/726,575
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1529
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-880-261-1

US-09-765-034-2 (1-334) x US-09-880-261-1 (1-1529)

Alignment Scores:
Pred. No.:
Score: 326.50
Percent Similarity: 47.55%
Best Local Similarity: 27.91%
Query Match: 18.69%
DB:

Length: 1529
Matches: 91
Conservative: 64
Mismatches: 134
Indels: 37
Gaps: 10

[Nucleotide/protein sequence alignment block — Qy (query) and Db (database) rows with match bars]

```
Db  1045 GCTGCAGTCTCTTCTTCATCCTGCTTCACTCCCATCATATTCATTTTATTTTTACACCATG 1104
          :::|||||||||||||||||||||:::
Qy   251 MetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThrGln 270
          |||||:|||:||||
Db  1105 GTAAAGGAAACCATCATTAGCAGT-------------------------TGTCCGGTT 1137

Qy   271 ValValIleAsnSerPheTyrIleValThrArgPro-----------LeuAlaPheLeu 286
          |||                                            |||||| |||
Db  1138 GTCCCAATCGCACTGTATTC--------CACCCTTTTGCCTGTTGCCTTGCCAAGTCTC 1188

Qy   287 AsnSerValIleAsnProValPheTyrPheLeuGlyAspHisPheArgAspMetLeu 306
          :::::|||:|||||||||||||||||||:::|||||:||||||||||| |||
Db  1189 TGCTGCCTTTTGGATCCAATTCTTTATTACTTTATGGCTTCAGAGTTTCGTTGACCAACTA 1248

Qy   307 MetAsnGlnLeuArgHis 312
          ||||||||||
Db  1249 TCC--------CGCCAT 1257
```

RESULT 15
US-09-852-156-7
Sequence 7, Application US/09852156
Patent No. US2002076694A1

GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:
  APPLICANT: Littman, Dan R.
      Deng, Hongkui
      Unutmaz, Derya
      Ramani, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
      ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
      IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
      THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
  ADDRESSEE: David A. Jackson, Esq.
  STREET: 411 Hackensack Ave, Continental Plaza, 4th
      Floor
  CITY: Hackensack
  STATE: New Jersey
  COUNTRY: USA
  ZIP: 07601

COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/852,156
  FILING DATE: 09-May-2001
  CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
  NAME: Jackson Esq., David A.
  REGISTRATION NUMBER: 26,742
  REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

TELECOMMUNICATION INFORMATION:
  TELEPHONE: 201-487-5800
  TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
  LENGTH: 1083 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
  ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-765-034-2 (1-334) x US-09-852-156-7 (1-1083)

```
Qy  25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValValGlyAsnThrIleVal 44
        ::::|||||   ::::||||||||    ||||||||||||||||||| :::::
Db 103 TTCCTTCCAGTCTTTTACATCGGTGTTCCTGACAGTGTGGGAAACCTTGTGTCTC 162

Qy  45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
        ::::||||||||| ||||||||   :::        ::::|||::::|||||||:::
Db 163 ATGGAGGCTTGCATTTCAAACCCGGCACGGCGAGACACTGATCGACATCTTTATCATCAAT 222

Qy  65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
        |||||:   |||||||||||||||| ||||||||:::::||||||||||
Db 223 CTGGGCTGCCTGCGACTTCATTTTGTTCGTCACATTGCCTCTCGTGGGGATAAAGAGCA 282

Qy 104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIle 123
        ::|||||||||| ||::::|||||||||||    |||    ||||||||||
Db 283 TCTCTAGGACTGTGGGAGGACGGCCTCCTTCCTGCAAAGGAGGCTTCTACAAGATCTCC 342

Qy 124 IleLysTyrProPheArgGluHisLeuLeuLysLysGluPheAlaIleLeuLeuIleSer 143
        :::|||     |||||||||||| ||||||||:::
Db 343 ACGGTCGATTGATGATAACCATACTGT--------GCAGAGAAAAGGCAACTCCAATT 402

Qy 144 LeuAlaIleLeuTrpValValThrLeuGluLeuProIleLeuProLeuAsnPro 163
        ::|||||||||||:::|||||||||||||||||:::::|||||||||:::
Db 403 ATTGTGTGGGCCAGTCGTATCCAGGAAAATTCAGGAGGACGAGCTGTGCAATATGTAGTTGT 462

Qy 164 ValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerGlyAspAsnTyr 183
        ::::::|||||||||||||::|||||||||::::
Db 463 GTCAATATGCACATGGCCAGTGTCCCTCCTGCTCACTTGCACTTGTGACCGTCTGGGAGGTC 522

Qy 184 AsnLeuIleTyrSerMetCysLeuThrLeuGlyPheLeuIlePheLeuIleProLeuPheValMet 203
        ::|||||||::|||    :::    |||||||||||||||||||:::
Db 523 ACCGTCGATTGATGATAACCATACTGT---------GCAGAGAAAAGGCAACTCCAATT 573

Qy 204 ----------CysPhePheTyrTyrLysIleAlaAlaGluPheLeuLysGlnArgAsnArg 219
                   ||| :::                |||    :::|||
Db 574 AAACTCATATGTGTCCCCGTGGCCTTAATTTCACCTTTTTGTCCCTTTTGTTGAGCATT 633

Qy 220 GlnValAlaThrAlaLeuProLeuGluGlyProLeuAsnLeuValIleMetAlaValVal 239
        :::|||||:::|||||||||||||||||:::::::
Db 634 GTGACCTGCTACTGTTGCATTGCAAGGAAGCTGTTGCCCAATTACCACCAATCAGGAAAG 693

Qy 240 IlePheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArg 259
        |||   |||||||||||:::::::       |||    :::|||
Db 694 CAC--------AACAAAAAGCTGAAGAAAATCTATAAAGGATCATCTTTATTGTCGTGGCA 744

Qy 260 LeuGlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleVal 279
        |||||::::::::::
Db 745 GCCTTTCTTGTCTCCTGGCCTGCCCTTCAAATACTTTACTTGGCCATTGTCTCTCT--- 801

Qy 280 ThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuGlyGly 299
        ::::|||||||||||||::::|||    :::|||||||||||||||||||
Db 802 --GGGTTGCGGCAAGAACATATTACCCCTGAGCTATTCTTCAGCGTTGGGTATGGAGGTG 858

Qy 300 AspHisPheArgAspMetLeuMetAsnGlnLeu--------------ArgHisAsnPhe 314
        |||                |||                             ::||||||| |||
Db 859 AGTGGACCCTTTGGCATTTGCCAACAGCTGTGTCAAACCCCTTTCAATTTACTAATACTTCGAC 918

Qy 315 LysSerLeuThrSerPheSer 321
        |||            :::|||
Db 919 AGCTACATCCCCGCGGCCATTGTCCACTGCTTGTTGCCCTTGCCTTGCCTGAAAAACTATGACTTT 978

Db 979 GGGAGTAGCACTGAGACATCA 999
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Query Match: 18.49%   Indels: 18
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Alignment Scores:
Pred. No.:
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